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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/985,675

DATE: 02/22/2002

TIME: 09:00:06

Input Set : N:\Crf3\RULE60\09985675.raw

Output Set: N:\CRF3\02222002\I985675.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: CROSIER, PHILIP S.

7 CROSIER, KATHRYN E.

9 (ii) TITLE OF INVENTION: DEVELOPMENTAL TYROSINE KINASES AND
10 THEIR LIGANDS

12 (iii) NUMBER OF SEQUENCES: 16

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: NIXON & VANDERHYE P.C.

16 (B) STREET: 1100 NORTH GLEBE ROAD

17 (C) CITY: ARLINGTON

18 (D) STATE: VIRGINIA

19 (E) COUNTRY: U.S.A.

20 (F) ZIP: 22201-4714

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/985,675

C--> 30 (B) FILING DATE: 05-Nov-2001

36 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US 08/505,241

35 (B) FILING DATE: 16-AUG-1995

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: MITCHARD, LEONARD C.

40 (B) REGISTRATION NUMBER: 29,009

41 (C) REFERENCE/DOCKET NUMBER: 175-19

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (703) 816-4000

45 (B) TELEFAX: (703) 816-4100

48 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 874 AMINO ACIDS

51 (B) TYPE: AMINO ACID

52 (D) TOPOLOGY: LINEAR

53 (ii) MOLECULE TYPE: PROTEIN

C--> 54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

55 Met	Gly	Trp	Pro	Gly	Leu	Arg	Pro	Leu	Leu	Leu	Ala	Gly
56 1					5				10			
57 Leu	Ala	Ser	Leu	Leu	Leu	Pro	Gly	Ser	Ala	Ala	Ala	Gly

ENTERED

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58	15	20	25
59 Leu	Lys Leu	Met Gly Ala	Pro Val Lys Met Thr Val Ser
60	30	35	
61 Gln	Gly Gln	Pro Val Lys	Leu Asn Cys Ser Val Glu Gly
62 40		45	50
63 Met	Glu Asp	Pro Asp Ile	His Trp Met Lys Asp Gly Thr
64	55	60	65
65 Val	Val Gln	Asn Ala Ser	Gln Val Ser Ile Ser Ile Ser
66	70	75	
67 Glu	His Ser	Trp Ile Gly	Leu Leu Ser Leu Lys Ser Val
68	80	85	90
69 Glu	Arg Ser	Asp Ala Gly	Leu Tyr Trp Cys Gln Val Lys
70	95	100	
71 Asp	Gly Glu	Glu Thr Lys	Ile Ser Gln Ser Val Trp Leu
72 105		110	115
73 Thr	Val Glu	Gly Val Pro	Phe Phe Thr Val Glu Pro Lys
74	120	125	130
75 Asp	Leu Ala	Val Pro Pro	Asn Ala Pro Phe Gln Leu Ser
76	135	140	
77 Cys	Glu Ala	Val Gly Pro	Pro Glu Pro Val Thr Ile Tyr
78	145	150	155
79 Trp	Trp Arg	Gly Leu Thr	Lys Val Gly Gly Pro Ala Pro
80	160	165	
81 Ser	Pro Ser	Val Leu Asn	Val Thr Gly Val Thr Gln Arg
82 170		175	180
83 Thr	Glu Phe	Ser Cys Glu	Ala Arg Asn Ile Lys Gly Leu
84	185	190	195
85 Ala	Thr Ser	Arg Pro Ala	Ile Val Arg Leu Gln Ala Pro
86	200	205	
87 Pro	Ala Ala	Pro Phe Asn	Thr Thr Val Thr Thr Ile Ser
88	210	215	220
89 Ser	Tyr Asn	Ala Ser Val	Ala Trp Val Pro Gly Ala Asp
90	225	230	
91 Gly	Leu Ala	Leu Leu His	Ser Cys Thr Val Gln Val Ala
92 235		240	245
93 His	Ala Pro	Gly Glu Trp	Glu Ala Leu Ala Val Val Val
94	250	255	260
95 Pro	Val Pro	Pro Phe Thr	Cys Leu Leu Arg Asn Leu Ala
96	265	270	
97 Pro	Ala Thr	Asn Tyr Ser	Leu Arg Val Arg Cys Ala Asn
98	275	280	285
99 Ala	Leu Gly	Pro Ser Pro	Tyr Gly Asp Trp Val Pro Phe
100	290	295	
101 Gln	Thr Lys	Gly Leu Ala	Pro Ala Arg Ala Pro Gln Asn
102 300		305	310
103 Phe	His Ala	Ile Arg Thr	Asp Ser Gly Leu Ile Leu Glu
104	315	320	325
105 Trp	Glu Glu	Val Ile Pro	Glu Asp Pro Gly Glu Gly Pro
106	330	335	

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107 Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly
108	340					345					350	
109 Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn
110			355					360				
111 Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg
112 365					370					375		
113 Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser
114		380					385				390	
115 Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg
116				395					400			
117 Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val
118		405				410					415	
119 Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala
120				420				425				
121 Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr
122 430					435					440		
123 Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly
124		445					450				455	
125 Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn
126				460					465			
127 Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser
128		470				475					480	
129 Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp
130				485				490				
131 Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met
132 495					500					505		
133 Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln
134		510					515				520	
135 Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val
136				525					530			
137 Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile
138		535				540					545	
139 Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe
140				550				555				
141 Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu
142 560					565					570		
143 Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val
144		575					580				585	
145 Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe
146				590						595		
147 Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu
148		600				605					610	
149 Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala
150				615				620				
151 Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His
152 625					630					635		
153 Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp
154		640					645				650	
155 Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys

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156			655			660		
157 Ile	Tyr Ser	Gly Asp	Tyr	Tyr Arg	Gln	Gly Cys	Ala Ser	
158	665			670			675	
159 Lys	Leu Pro	Val Lys	Trp	Leu Ala	Leu	Glu Ser	Leu Ala	
160		680			685			
161 Asp	Asn Leu	Tyr Thr	Val	His Ser	Asp	Val Trp	Ala Phe	
162 690			695			700		
163 Gly	Val Thr	Met Trp	Glu	Ile Met	Thr	Arg Gly	Gln Thr	
164	705			710			715	
165 Pro	Tyr Ala	Gly Ile	Glu	Asn Ala	Glu	Ile Tyr	Asn Tyr	
166		720				725		
167 Leu	Ile Gly	Gly Asn	Arg	Leu Lys	Gln	Pro Pro	Glu Cys	
168	730			735			740	
169 Met	Glu Glu	Val Tyr	Asp	Leu Met	Tyr	Gln Cys	Trp Ser	
170		745			750			
171 Ala	Asp Pro	Lys Gln	Arg	Pro Ser	Phe	Thr Cys	Leu Arg	
172 755			760			765		
173 Met	Glu Leu	Glu Asn	Ile	Leu Gly	His	Leu Ser	Val Leu	
174	770			775			780	
175 Ser	Thr Ser	Gln Asp	Pro	Leu Tyr	Ile	Asn Ile	Glu Arg	
176		785				790		
177 Ala	Glu Gln	Pro Thr	Glu	Ser Gly	Ser	Pro Glu	Leu His	
178	795			800			805	
179 Cys	Gly Glu	Arg Ser	Ser	Ser Glu	Ala	Gly Asp	Gly Ser	
180		810			815			
181 Gly	Val Gly	Ala Val	Gly	Gly Ile	Pro	Ser Asp	Ser Arg	
182 820			825			830		
183 Tyr	Ile Phe	Ser Pro	Gly	Gly Leu	Ser	Glu Ser	Pro Gly	
184	835			840			845	
185 Gln	Leu Glu	Gln Gln	Pro	Glu Ser	Pro	Leu Asn	Glu Asn	
186		850				855		
187 Gln	Arg Leu	Leu Leu	Leu	Gln Gln	Gly	Leu Leu	Pro His	
188	860			865			870	
189 Ser	Ser Cys							

C--> 192 (2) INFORMATION FOR SEQ ID NO: 2:

193 (i) SEQUENCE CHARACTERISTICS:

194 (A) LENGTH: 850 AMINO ACIDS

195 (B) TYPE: AMINO ACID

C--> 196 (D) TOPOLOGY: LINEAR

197 (ii) MOLECULE TYPE: PROTEIN

C--> 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

199								Ala Gly
200								1
201 Leu	Lys Leu	Met Gly	Ala	Pro Val	Lys	Met Thr	Val Ser	
202	5			10				15
203 Gln	Gly Gln	Pro Val	Lys	Leu Asn	Cys	Ser Val	Glu Gly	
204		20				25		
205 Met	Glu Asp	Pro Asp	Ile	His Trp	Met	Lys Asp	Gly Thr	
206	30			35			40	

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207 Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser
208			45					50				
209 Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val
210 55					60					65		
211 Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys
212		70					75					80
213 Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu
214				85						90		
215 Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys
216		95					100					105
217 Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser
218			110					115				
219 Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr
220 120					125					130		
221 Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro
222		135					140					145
223 Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg
224				150						155		
225 Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu
226		160					165					170
227 Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro
228			175					180				
229 Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser
230 185					190					195		
231 Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp
232		200					205					210
233 Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala
234				215						220		
235 His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val
236		225					230					235
237 Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala
238			240					245				
239 Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn
240 250					255					260		
241 Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe
242		265					270					275
243 Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn
244				280						285		
245 Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu
246		290					295					300
247 Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro
248			305					310				
249 Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly
250 315					320					325		
251 Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn
252		330					335					340
253 Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg
254				345						350		
255 Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/985,675

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TIME: 09:00:07

Input Set : N:\Crif3\RULE60\09985675.raw

Output Set: N:\CRF3\02222002\I985675.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:52 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:54 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:192 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:196 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:198 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:335 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:339 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:341 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:479 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:483 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:485 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:620 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:624 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:626 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:691 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:695 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:697 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
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L:768 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
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L:984 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
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L:1091 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
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L:1105 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1112 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1117 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1124 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1129 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1136 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]